

SEQUENCE LISTING



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Spendlove, Ian
Hewett, Peter W
Ramage, Judith M

<120> Anti-angiogenic vaccines: substances and methods
relating thereto

<130> 0380-P02286US0

<140> US 09/623,063

<141> 2000-10-24

<150> PCT/GB99/00583

<151> 1999-02-26

<150> GB 9804121.3

<151> 1998-02-26

<160> 17

<170> PatentIn Ver. 2.1

<210> 1

<211> 1124

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Sequence source
uncertain

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Met Asp Ser Leu Ala Ser Leu Val Leu Cys Gly Val Ser Leu Leu Leu
1 5 10 15

Ser Gly Thr Val Glu Gly Ala Met Asp Leu Ile Leu Ile Asn Ser Leu
20 25 30

Pro Leu Val Ser Asp Ala Glu Thr Ser Leu Thr Cys Ile Ala Ser Gly
35 40 45

Trp Arg Pro His Glu Pro Ile Thr Ile Gly Arg Asp Phe Glu Ala Leu
50 55 60

Met Asn Gln His Gln Asp Pro Leu Glu Val Thr Gln Asp Val Thr Arg
65 70 75 80

Glu Trp Ala Lys Lys Val Val Trp Lys Arg Glu Lys Ala Ser Lys Ile
85 90 95

Asn Gly Ala Tyr Phe Cys Glu Gly Arg Val Arg Gly Glu Ala Ile Arg
100 105 110

Ile Arg Thr Met Lys Met Arg Gln Gln Ala Ser Phe Leu Pro Ala Thr
115 120 125

Leu Thr Met Thr Val Asp Lys Gly Asp Asn Val Asn Ile Ser Phe Lys
130 135 140

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Lys Val Leu Ile Lys Glu Glu Asp Ala Val Ile Tyr Lys Asn Gly Ser
 145 150 155 160
 Phe Ile His Ser Val Pro Arg His Glu Val Pro Asp Ile Leu Glu Val
 165 170 175
 His Leu Pro His Ala Gln Pro Gln Asp Ala Gly Val Tyr Ser Ala Arg
 180 185 190
 Tyr Ile Gly Gly Asn Leu Phe Thr Ser Ala Phe Thr Arg Leu Ile Val
 195 200 205
 Arg Arg Cys Glu Ala Gln Lys Trp Gly Pro Glu Cys Asn His Leu Cys
 210 215 220
 Thr Ala Cys Met Asn Asn Gly Val Cys His Glu Asp Thr Gly Glu Cys
 225 230 235 240
 Ile Cys Pro Pro Gly Phe Met Gly Arg Thr Cys Glu Lys Ala Cys Glu
 245 250 255
 Leu His Thr Phe Gly Arg Thr Cys Lys Glu Arg Cys Ser Gly Gln Glu
 260 265 270
 Gly Cys Lys Ser Tyr Val Phe Cys Leu Pro Asp Pro Tyr Gly Cys Ser
 275 280 285
 Cys Ala Thr Gly Trp Lys Gly Leu Gln Cys Asn Glu Ala Cys His Pro
 290 295 300
 Gly Phe Tyr Gly Pro Asp Cys Lys Leu Arg Cys Ser Cys Asn Asn Gly
 305 310 315 320
 Glu Met Cys Asp Arg Phe Gln Gly Cys Leu Cys Ser Pro Gly Trp Gln
 325 330 335
 Gly Leu Gln Cys Glu Arg Glu Gly Ile Pro Arg Met Thr Pro Lys Ile
 340 345 350
 Val Asp Leu Pro Asp His Ile Glu Val Asn Ser Gly Lys Phe Asn Pro
 355 360 365
 Ile Cys Lys Ala Ser Gly Trp Pro Leu Pro Thr Asn Glu Glu Met Thr
 370 375 380
 Leu Val Lys Pro Asp Gly Thr Val Leu His Pro Lys Asp Phe Asn His
 385 390 395 400
 Thr Asp His Phe Ser Val Ala Ile Phe Thr Ile His Arg Ile Leu Pro
 405 410 415
 Pro Asp Ser Gly Val Trp Val Cys Ser Val Asn Thr Val Ala Gly Met
 420 425 430
 Val Glu Lys Pro Phe Asn Ile Ser Val Lys Val Leu Pro Lys Pro Leu
 435 440 445
 Asn Ala Pro Asn Val Ile Asp Thr Gly His Asn Phe Ala Val Ile Asn
 450 455 460
 Ile Ser Ser Glu Pro Tyr Phe Gly Asp Gly Pro Ile Lys Ser Lys Lys
 465 470 475 480

Leu Leu Tyr Lys Pro Val Asn His Tyr Glu Ala Trp Gln His Ile Gln
 485 490
 Val Thr Asn Glu Ile Val Thr Leu Asn Tyr Leu Glu Pro Arg Thr Glu
 500 505 510
 Tyr Glu Leu Cys Val Gln Leu Val Arg Arg Gly Glu Gly Gly Glu Gly
 515 520 525
 His Pro Gly Pro Val Arg Arg Phe Thr Thr Ala Ser Ile Gly Leu Pro
 530 535 540
 Pro Pro Arg Gly Leu Asn Leu Leu Pro Lys Ser Gln Thr Thr Leu Asn
 545 550 555 560
 Leu Thr Trp Gln Pro Ile Phe Pro Ser Ser Glu Asp Asp Phe Tyr Val
 565 570 575
 Glu Val Glu Arg Arg Ser Val Gln Lys Ser Asp Gln Gln Asn Ile Lys
 580 585 590
 Val Pro Gly Asn Leu Thr Ser Val Leu Leu Asn Asn Leu His Pro Arg
 595 600 605
 Glu Gln Tyr Val Val Arg Ala Arg Val Asn Thr Lys Ala Gln Gly Glu
 610 615 620
 Trp Ser Glu Asp Leu Thr Ala Trp Thr Leu Ser Asp Ile Leu Pro Pro
 625 630 635 640
 Gln Pro Glu Asn Ile Lys Ile Ser Asn Ile Thr His Ser Ser Ala Val
 645 650 655
 Ile Ser Trp Thr Thr Ile Leu Asp Gly Tyr Ser Ile Ser Ser Ile Thr Ile
 660 665 670
 Arg Tyr Lys Val Gln Gly Lys Asn Glu Asp Gln His Val Asp Val Lys
 675 680 685
 Ile Lys Asn Ala Thr Ile Ile Gln Tyr Gln Leu Lys Gly Leu Glu Pro
 690 695 700
 Glu Thr Ala Tyr Gln Val Asp Ile Phe Ala Glu Asn Asn Ile Gly Ser
 705 710 715 720
 Ser Asn Pro Ala Phe Ser His Glu Leu Val Thr Leu Pro Glu Ser Gln
 725 730 735
 Ala Pro Ala Asp Leu Gly Gly Gly Lys Met Leu Leu Ile Ala Ile Leu
 740 745 750
 Gly Ser Ala Gly Met Thr Cys Leu Thr Val Leu Leu Ala Phe Leu Ile
 755 760 765
 Ile Leu Gln Leu Lys Arg Ala Asn Val Gln Arg Arg Met Ala Gln Ala
 770 775 780
 Phe Gln Asn Val Arg Glu Glu Pro Ala Val Gln Phe Asn Ser Gly Thr
 785 790 795 800
 Leu Ala Leu Asn Arg Lys Val Lys Asn Asn Pro Asp Pro Thr Ile Tyr
 805 810 815

Pro Val Leu Asp Trp Asn Asp Ile Lys Phe Gln Asp Val Ile Gly Glu
 820 825 830
 Gly Asn Phe Gly Gln Val Leu Lys Ala Arg Ile Lys Lys Asp Gly Leu
 835 840 845
 Arg Met Asp Ala Ala Ile Lys Arg Met Lys Glu Tyr Ala Ser Lys Asp
 850 855 860
 Asp His Arg Asp Phe Ala Gly Glu Leu Glu Val Leu Cys Lys Leu Gly
 865 870 875 880
 His His Pro Asn Ile Ile Asn Leu Leu Gly Ala Cys Glu His Arg Gly
 885 890 895
 Tyr Leu Tyr Leu Ala Ile Glu Tyr Ala Pro His Gly Asn Leu Leu Asp
 900 905 910
 Phe Leu Arg Lys Ser Arg Val Leu Glu Thr Asp Pro Ala Phe Ala Ile
 915 920 925
 Ala Asn Ser Thr Ala Ser Thr Leu Ser Ser Gln Gln Leu Leu His Phe
 930 935 940
 Ala Ala Asp Val Ala Arg Gly Met Asp Tyr Leu Ser Gln Lys Gln Phe
 945 950 955 960
 Ile His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Gly Glu Asn Tyr
 965 970 975
 Val Ala Lys Ile Ala Asp Phe Gly Leu Ser Arg Gly Gln Glu Val Tyr
 980 985 990
 Val Lys Lys Thr Met Gly Arg Leu Pro Val Arg Trp Met Ala Ile Glu
 995 1000 1005
 Ser Leu Asn Tyr Ser Val Tyr Thr Thr Asn Ser Asp Val Trp Ser Tyr
 1010 1015 1020
 Gly Val Leu Leu Trp Glu Ile Val Ser Leu Gly Gly Thr Pro Tyr Cys
 1025 1030 1035 1040
 Gly Met Thr Cys Ala Glu Leu Tyr Glu Lys Leu Pro Gln Gly Tyr Arg
 1045 1050 1055
 Leu Glu Lys Pro Leu Asn Cys Asp Asp Glu Val Tyr Asp Leu Met Arg
 1060 1065 1070
 Gln Cys Trp Arg Glu Lys Pro Tyr Glu Arg Pro Ser Phe Ala Gln Ile
 1075 1080 1085
 Leu Val Ser Leu Asn Arg Met Leu Glu Glu Arg Lys Thr Tyr Val Asn
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 Thr Thr Leu Tyr Glu Lys Phe Thr Tyr Ala Gly Ile Asp Cys Ser Ala
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 Glu Glu Ala Ala

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 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Sequence source
 uncertain

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 Leu Thr Asp Pro Gln Arg Phe Phe Leu Thr Cys Val Ser Gly Glu Ala
 35 40 45
 Gly Ala Gly Arg Gly Ser Asp Ala Trp Gly Pro Pro Leu Leu Leu Glu
 50 55 60
 Lys Asp Asp Arg Ile Val Arg Thr Pro Pro Gly Pro Pro Leu Arg Leu
 65 70 75 80
 Ala Arg Asn Gly Ser His Gln Val Thr Leu Arg Gly Phe Ser Lys Pro
 85 90 95
 Ser Asp Leu Val Gly Val Phe Ser Cys Val Gly Gly Ala Gly Ala Arg
 100 105 110
 Arg Thr Arg Val Ile Tyr Val His Asn Ser Pro Gly Ala His Leu Leu
 115 120 125
 Pro Asp Lys Val Thr His Thr Val Asn Lys Gly Asp Thr Ala Val Leu
 130 135 140
 Ser Ala Arg Val His Lys Glu Lys Gln Thr Asp Val Ile Trp Lys Ser
 145 150 155 160
 Asn Gly Ser Tyr Phe Tyr Thr Leu Asp Trp His Glu Ala Gln Asp Gly
 165 170 175
 Arg Phe Leu Leu Gln Leu Pro Asn Val Gln Pro Pro Ser Ser Gly Ile
 180 185 190
 Tyr Ser Ala Thr Tyr Leu Glu Ala Ser Pro Leu Gly Ser Ala Phe Phe
 195 200 205
 Arg Leu Ile Val Arg Gly Cys Gly Ala Gly Arg Trp Gly Pro Gly Cys
 210 215 220
 Thr Lys Glu Cys Pro Gly Cys Leu His Gly Gly Val Cys His Asp His
 225 230 235 240
 Asp Gly Glu Cys Val Cys Pro Pro Gly Phe Thr Gly Thr Arg Cys Glu
 245 250 255
 Gln Ala Cys Arg Glu Gly Arg Phe Gly Gln Ser Cys Gln Glu Gln Cys
 260 265 270
 Pro Gly Ile Ser Gly Cys Arg Gly Leu Thr Phe Cys Leu Pro Asp Pro
 275 280 285

Tyr Gly Cys Ser Cys Gly Ser Gly Trp Arg Gly Ser Gln Cys Gln Glu
 290 295 300
 Ala Cys Ala Pro Gly His Phe Gly Ala Asp Cys Arg Leu Gln Cys Gln
 305 310 315 320
 Cys Gln Asn Gly Gly Thr Cys Asp Arg Phe Ser Gly Cys Val Cys Pro
 325 330 335
 Ser Gly Trp His Gly Val His Cys Glu Lys Ser Asp Arg Ile Pro Gln
 340 345 350
 Ile Leu Asn Met Ala Ser Glu Leu Glu Phe Asn Leu Glu Thr Met Pro
 355 360 365
 Arg Ile Asn Cys Ala Ala Ala Gly Asn Pro Phe Pro Val Arg Gly Ser
 370 375 380
 Ile Glu Leu Arg Lys Pro Asp Gly Thr Val Leu Leu Ser Thr Lys Ala
 385 390 395 400
 Ile Val Glu Pro Glu Lys Thr Thr Ala Glu Phe Glu Val Pro Arg Leu
 405 410 415
 Val Leu Ala Asp Ser Gly Phe Trp Glu Cys Arg Val Ser Thr Ser Gly
 420 425 430
 Gly Gln Asp Ser Arg Arg Phe Lys Val Asn Val Lys Val Pro Pro Val
 435 440 445
 Pro Leu Ala Ala Pro Arg Leu Leu Thr Lys Gln Ser Arg Gln Leu Val
 450 455 460
 Val Ser Pro Leu Val Ser Phe Ser Gly Asp Gly Pro Ile Ser Thr Val
 465 470 475 480
 Arg Leu His Tyr Arg Pro Gln Asp Ser Thr Met Asp Trp Ser Thr Ile
 485 490 495
 Val Val Asp Pro Ser Glu Asn Val Thr Leu Met Asn Leu Arg Pro Lys
 500 505 510
 Thr Gly Tyr Ser Val Arg Val Gln Leu Ser Arg Pro Gly Glu Gly Gly
 515 520 525
 Glu Gly Ala Trp Gly Pro Pro Thr Leu Met Thr Thr Asp Cys Pro Glu
 530 535 540
 Pro Leu Leu Gln Pro Trp Leu Glu Gly Trp His Val Glu Gly Thr Asp
 545 550 555 560
 Arg Leu Arg Val Ser Trp Ser Leu Pro Leu Val Pro Gly Pro Leu Val
 565 570 575
 Gly Asp Gly Phe Leu Leu Arg Leu Trp Asp Gly Thr Arg Gly Gln Glu
 580 585 590
 Arg Arg Glu Asn Val Ser Ser Pro Gln Ala Arg Thr Ala Leu Leu Thr
 595 600 605
 Gly Leu Thr Pro Gly Thr His Tyr Gln Leu Asp Val Gln Leu Tyr His
 610 615 620

Cys Thr Leu Leu Gly Pro Ala Ser Pro Pro Ala His Val Leu Leu Pro
 625 630 635 640
 Pro Ser Gly Pro Pro Ala Pro Arg His Leu His Ala Gln Ala Leu Ser
 645 650 655
 Asp Ser Glu Ile Gln Leu Thr Trp Lys His Pro Glu Ala Leu Pro Gly
 660 665 670
 Pro Ile Ser Lys Tyr Val Val Glu Val Gln Val Ala Gly Gly Ala Gly
 675 680 685
 Asp Pro Leu Trp Ile Asp Val Asp Arg Pro Glu Glu Thr Ser Thr Ile
 690 695 700
 Ile Arg Gly Leu Asn Ala Ser Thr Arg Tyr Leu Phe Arg Met Arg Ala
 705 710 715 720
 Ser Ile Gln Gly Leu Gly Asp Trp Ser Asn Thr Val Glu Glu Ser Thr
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 Leu Gly Asn Gly Leu Gln Ala Glu Gly Pro Val Gln Glu Ser Arg Ala
 740 745 750
 Ala Glu Glu Gly Leu Asp Gln Gln Leu Ile Leu Ala Val Val Gly Ser
 755 760 765
 Val Ser Ala Thr Cys Leu Thr Ile Leu Ala Ala Leu Leu Thr Leu Val
 770 775 780
 Cys Ile Arg Arg Ser Cys Leu His Arg Arg Arg Thr Phe Thr Tyr Gln
 785 790 795 800
 Ser Gly Ser Gly Glu Glu Thr Ile Leu Gln Phe Ser Ser Gly Thr Leu
 805 810 815
 Thr Leu Thr Arg Arg Pro Lys Leu Gln Pro Glu Pro Leu Ser Tyr Pro
 820 825 830
 Val Leu Glu Trp Glu Asp Ile Thr Phe Glu Asp Leu Ile Gly Glu Gly
 835 840 845
 Asn Phe Gly Gln Val Ile Arg Ala Met Ile Lys Lys Asp Gly Leu Lys
 850 855 860
 Met Asn Ala Ala Ile Lys Met Leu Lys Glu Tyr Ala Ser Glu Asn Asp
 865 870 875 880
 His Arg Asp Phe Ala Gly Glu Leu Glu Val Leu Cys Lys Leu Gly His
 885 890 895
 His Pro Asn Ile Ile Asn Leu Leu Gly Ala Cys Lys Asn Arg Gly Tyr
 900 905 910
 Leu Tyr Ile Ala Ile Glu Tyr Ala Pro Tyr Gly Asn Leu Leu Asp Phe
 915 920 925
 Leu Arg Lys Ser Arg Val Leu Glu Thr Asp Pro Ala Phe Ala Arg Glu
 930 935 940
 His Gly Thr Ala Ser Thr Leu Ser Ser Arg Gln Leu Leu Arg Phe Ala
 945 950 955 960

Ser Asp Ala Ala Asn Gly Met Gln Tyr Leu Ser Glu Lys Gln Phe Ile
 965 970 975
 His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Gly Glu Asn Leu Ala
 980 985 990
 Ser Lys Ile Ala Asp Phe Gly Leu Ser Arg Gly Glu Glu Val Tyr Val
 995 1000 1005
 Lys Lys Thr Met Gly Arg Leu Pro Val Arg Trp Met Ala Ile Glu Ser
 1010 1015 1020
 Leu Asn Tyr Ser Val Tyr Thr Thr Lys Ser Asp Val Trp Ser Phe Gly
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 Val Leu Leu Trp Glu Ile Val Ser Leu Gly Gly Thr Pro Tyr Cys Gly
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 Met Thr Cys Ala Glu Leu Tyr Glu Lys Leu Pro Gln Gly Tyr Arg Met
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 Glu Gln Pro Arg Asn Cys Asp Asp Glu Val Tyr Glu Leu Met Arg Gln
 1075 1080 1085
 Cys Trp Arg Asp Arg Pro Tyr Glu Arg Pro Pro Phe Ala Gln Ile Ala
 1090 1095 1100
 Leu Gln Leu Gly Arg Met Leu Glu Ala Arg Lys Ala Tyr Val Asn Met
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 Ser Leu Phe Glu Asn Phe Thr Tyr Ala Gly Ile Asp Ala Thr Ala Glu
 1125 1130 1135

Glu Ala

<210> 3
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 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Sequence source
 uncertain

<400> 3
 Gly Met Val Glu Lys Pro Phe Asn Ile
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<210> 4
 <211> 9
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Sequence source
 uncertain

<400> 4
 Arg Met Thr Pro Lys Ile Val Asp Leu
 1 5

<210> 5
 <211> 9
 <212> PRT
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 <220>
 <223> Description of Unknown Organism: Sequence source
 uncertain

 <400> 5
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 <210> 6
 <211> 9
 <212> PRT
 <213> Unknown Organism

 <220>
 <223> Description of Unknown Organism: Sequence source
 uncertain

 <400> 6
 Thr Ile Gly Arg Asp Phe Glu Ala Leu
 1 5

 <210> 7
 <211> 9
 <212> PRT
 <213> Unknown Organism

 <220>
 <223> Description of Unknown Organism: Sequence source
 uncertain

 <400> 7
 Asn Gln His Gln Asp Pro Leu Glu Val
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 <210> 8
 <211> 9
 <212> PRT
 <213> Unknown Organism

 <220>
 <223> Description of Unknown Organism: Sequence source
 uncertain

 <400> 8
 Pro Arg His Glu Val Pro Asp Ile Leu
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 <210> 9
 <211> 9
 <212> PRT
 <213> Unknown Organism

 <220>
 <223> Description of Unknown Organism: Sequence source

uncertain

<400> 9

Lys Ile Val Asp Leu Pro Asp His Ile
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<210> 10

<211> 10

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Sequence source
uncertain

<400> 10

Gly Ile Pro Arg Met Thr Pro Lys Ile Val
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<210> 11

<211> 9

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Sequence source
uncertain

<400> 11

Asn Leu His Pro Arg Glu Gln Tyr Val
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<210> 12

<211> 9

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Sequence source
uncertain

<400> 12

Ile Leu Ile Asn Ser Leu Pro Leu Val
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<210> 13

<211> 10

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Sequence source
uncertain

<400> 13

Ile Val Asp Leu Pro Asp His Ile Glu Val
1 5 10

<210> 14
 <211> 20
 <212> PRT
 <213> Unknown Organism

 <220>
 <223> Description of Unknown Organism: Sequence source
 uncertain

 <400> 14
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 1 5 10 15

 Pro Leu Glu Val
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 <210> 15
 <211> 57
 <212> PRT
 <213> Unknown Organism

 <220>
 <223> Description of Unknown Organism: Sequence source
 uncertain

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 1 5 10 15

 Ile Gly Arg Asp Phe Glu Ala Leu Met Asn Gln His Gln Asp Pro Leu
 20 25 30

 Glu Val Thr Gln Asp Val Thr Arg Glu Trp Ala Lys Lys Val Val Trp
 35 40 45

 Lys Arg Glu Lys Ala Ser Lys Ile Asn
 50 55

 <210> 16
 <211> 10
 <212> PRT
 <213> Unknown Organism

 <220>
 <223> Description of Unknown Organism: Sequence source
 uncertain

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 Phe Leu Pro Ser Asp Phe Phe Pro Ser Val
 1 5 10

 <210> 17
 <211> 9
 <212> PRT
 <213> Unknown Organism

 <220>
 <223> Description of Unknown Organism: Sequence source
 uncertain

<400> 17
Glu Val Asp Pro Ile Gly His Leu Tyr
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